REMARKS

Claims 2, 3, 6, 7, 9, 10, 12, 13, 15, 16, and 18-24 are pending in the present application.

The rejection of Claims 2, 3, 6, 7, 9, 10, 12, 13, 15, 16, and 18-25 under 35 U.S.C. §112, first paragraph ("written description"), is respectfully traversed.

In making this ground of rejection, the Examiner alleges that the claims are directed toward any argR gene of any coryneform bacterium. However, Applicants remind the Examiner that the present invention provides, *inter alia*, an isolated coryneform bacterium wherein an argR gene on a chromosome of the bacterium is disrupted, and the argR gene prior to being disrupted has the nucleotide sequence shown in SEQ ID NO:17 (see Claim 2). Accordingly, the nucleotide sequence of the argR gene prior to being disrupted has the nucleotide sequence shown in SEQ ID NO:17. Applicants submit that the allegation by the Examiner is contradictory to the invention as claimed, because the claims are not directed toward any argR gene but rather embrace disruption mutants of the argR sequence defined in SEQ ID NO: 17. Therefore, this criticism by the Examiner is without merit and should be withdrawn.

The Examiner further asserts that there is no known or disclosed correlation between the coding region of a polynucleotide encoding the argR argnine repressor and the structure of the non-described promoter region, regulatory elements, and untranslated regions of the gene.

On the contrary, the nucleotide sequence of a DNA fragment containing the argR gene is described in the specification (i.e., SEQ ID NO: 17). The position and structure of the coding region of the argR gene are also well described in the specification and Sequence Listing (see CD region defined in SEQ ID NO: 17 (res. 1852 to 2364) and the resultant gene product set

forth in SEQ ID NO: 18). Therefore, Applicants submit that the skilled artisan would readily appreciate the sequence of the untranslated regions, as well as that of the coding region. Further, the skilled artisan with SEQ ID NO: 17 in hand would be able to surmise the promoter region based on the sequence of the coding region and the untranslated region 5'-thereof. Moreover, the disrupted argR gene would be readily appreciated by the skilled artisan, as well as methods of modification thereof and/or methods of identifying such sequences.

As for a modified protein that is imparted with positive properties, including increased specific activity or heat stability, it is understandable how the Examiner may allege that such a protein is not sufficiently described absent a definition of the specific structure and/or mutations. However, in the present application the claimed sequence is disrupted and, thus, resulting in a protein that is non-functional or difficult to express (see pages 10-13). Such a disruption can by one of several mechanisms, each of which is known by the skilled artisan. For example, the polynucleotide of SEQ ID NO: 17 may be disrupted by deleting a substantial part of the coding region or the promoter region.

In view of the foregoing, Applicants submit that the present invention is sufficiently described within the context of 35 U.S.C. §112, first paragraph. Applicants request withdrawal of this ground of rejection.

The objection of Claim 25 under 37 C.F.R. §1.75 as being a substantial duplicate of Claim 24 is obviated by cancellation of Claim 25. Acknowledgement that this ground of objection has been withdrawn is requested.

Applicants submit that the present application is now in condition for allowance. Early notification of such action is earnestly solicited.

Respectfully submitted,

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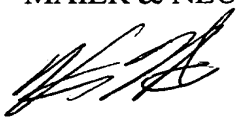

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